IN THE SPECIFICATION

Please replace the text beginning at page 18, line 8 through page 19, line 13, with the following rewritten text:

- Figure 7:

~~(a)~~ (A) : Localization of the genes vanR, vanS, vanes, vanA, vanX, vanY, vanZ of the gene for the transposase and of the gene for the resolvase as well as the repeated reverse terminal sequences of 38 bp at the end of the transposon.

~~(b) :~~ Mapping of the plasmids. ~~(A)~~ (B) Polylinker pAT29 and derivatives constructed in this study. The arrow labelled P2 indicates the position and orientation of the P2 promoter of aphA-3 (Caillaud et al., 1987, Mol. Gen. Genet. 207:509-513). ~~(B)~~ (C) Insert pAT80. The white rectangles indicate the DNA of pAT29 but they are not shown to scale. The rectangles terminating in an arrow indicate the coding sequences. The arrows shown in vertical and horizontal full lines indicate the position and orientation, respectively, of the apha-1 gene in the derivatives of pAT80. Restriction sites: Ac, AccI; B, BamHI; Bg, Bg1II; Bs, BssHII; E, EcoRI; H, HindIII; Hc, HincII; K, KpnI; P, PstI; S, SmaI; SI, SacI, SII, SacII; Sa, SalI; Sp, SphI; Xb, XbaI. ~~(C)~~ (D) Inserts in pAT86, pAT87, pAT88 and pAT89. The inserts are shown by full lines and the corresponding vectors are indicated in parentheses.

- Figure 8 A-W: nucleotide sequence of the transposon shown in Figure 7 and amino acid sequence of the corresponding proteins. The nucleotide sequence is shown for the (+) strand and for the (-) strand (corresponding to the complementary sequence of the (+) strand for the positions 1 to 3189) on which the coding sequence of the transposase is located.

- Figure 9 A-C: Nucleotide sequence of the SacI-PstI fragment of 1347 bp of the plasmid pAT216 containing the vanC gene. The numbering starts at the first base G of the SacI restriction site. The potential RBS sequence upstream from the initiation codon ATG of translation at position 215 is underlined. The STOP codon (TGA) is indicated by *. The

region coding for the vanC and the deduced amino acid sequence are indicated in bold characters. Sequential overlapping clones were generated by restriction fragments of subcloning of pAT216 in the bacteriophage M13mp10 (Amersham, England). The universal primer (New England Biolabs Beverly MA) was used to sequence the insert in the recombinant phages. The sequencing was performed by the enzymatic dideoxy nucleotide method (Sanger et al., 1977 PNAS 74: 5463-5467) by using the T7 DNA polymerase (Sequenase US B CORP, Cleveland, OH) and [x-35 S] dATP (Amersham, England). The reaction products were loaded onto 6% denaturing polyacrylamide gels.